SEQUENCE LISTING

<110> Kornbluth, Richard S

<120> Multimeric forms of CD40L and other TNF family members

<130> TNFSF-collectin fusion proteins

<140> 60/111,471
<141> 1998-12-08

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<170> PatentIn Ver. 2.1

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<223> Mature murine surfactant protein D including hub region, collagenous portion, and neck, but excluding carbohydrate recognition domain (CRD)

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<223> Human CD40 ligand extracellular region, including stalk.

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<223> Description of Artificial Sequence: Murine

surfactant protein D (without the CRD) fused to
the extracellular portion of human CD40L

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<301> Spriggs, Melanie K.
Armitage, Richard J.
Strockbine, L
Clifford, K N.
Macduff, B M.
Sato, T A.
Maliszewski, C R.
Fanslow, William C.
<302> Recombinant human CD40 ligand stimulates B cell
proliferation and immunoglobulin E secretion.
<303> J. Exp. Med.
<304> 176
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<306> 1543-1550
<307> 1992
<313> 801 TO 1600

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White, R A.
<302> Mouse surfactant protein-D. cDNA cloning,
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<303> J. Immunol.
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ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga   292
Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
             75                  80                  85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta   340
Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
         90                  95                 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa   388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
    105                 110                 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt   436
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120                 125                 130                 135

cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg   484
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
                140                 145                 150

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Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
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        170                 175                 180

cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc   628
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro
    185                 190                 195

cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa   676
Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys
200                 205                 210                 215

ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag   724
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<223> Description of Artificial Sequence: Murine surfactant protein D (without the CRD) fused to the extracellular portion of human CD40L

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Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
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Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
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Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
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Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
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Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

His Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
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Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
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Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
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Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
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Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
325 330 335

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
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Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
370 375 380

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<223> Murine RANKL/TRANCE extracellular region,
including stalk

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White, R A.
Guo, N
Dowler, L L.
Tauber, A I.
Motwani, M
<302> Mouse surfactant protein-D. cDNA cloning,
characterization, and gene localization to chromosome
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<303> J. Immunol.
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<307> 1995
<313> 32 TO 800

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<301> Anderson, D M.
Maraskovsky, E
Billingsley, W L.
Dougall, W C.
<302> A homologue of the TNF receptor and its ligand enhance
T-cell growth and dendritic-cell function.
<303> Nature
<304> 390
<305> 6656
<306> 175-179
<307> 1997
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 40                  45                  50                  55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg   244
Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
                 60                  65                  70

ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga   292
Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
             75                  80                  85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta   340
Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
         90                  95                 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa   388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
    105                 110                 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt   436
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120                 125                 130                 135

cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg   484
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
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caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga   532
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
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Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly
        170                 175                 180

cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc   628
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro
    185                 190                 195

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Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys
200                 205                 210                 215

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            235                 240                 245

cag aaa gct gca ttg ttc cct gat ggt cga gcg cag atg gat cct aac   820
Gln Lys Ala Ala Leu Phe Pro Asp Gly Arg Ala Gln Met Asp Pro Asn
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aga ata tca gaa gac agc act cac tgc ttt tat aga atc ctg aga ctc   868
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cat gaa aac gca ggt ttg cag gac tcg act ctg gag agt gaa gac aca   916
His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr
280                 285                 290                 295

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                300                 305                 310

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360                 365                 370                 375

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Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg
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gtt aac caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg  1252
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            395                 400                 405

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    425                 430                 435

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Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His
440                 445                 450                 455

ttt tat tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa   1444
Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu
                460                 465                 470

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             20                  25                  30

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         35                  40                  45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
     50                  55                  60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
 65                  70                  75                  80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
                 85                  90                  95
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Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
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Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys
260 265 270

Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser
275 280 285

Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys
290 295 300

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
305 310 315 320

Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu
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Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu
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Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu
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Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu
385                 390                 395                 400

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro
                405                 410                 415

Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys
            420                 425                 430

Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp
        435                 440                 445

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
    450                 455                 460

Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro
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<223> Mature murine surfactant protein D including hub region, collagenous portion, and neck, but excluding carbohydrate recognition domain (CRD)

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Guo, N
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Motwani, M
<302> Mouse surfactant protein-D. cDNA cloning, characterization, and gene localization to chromosome 14.
<303> J. Immunol.
<304> 155
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<307> 1995
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Fanslow, W
Sato, T A.
Clifford, K N.
<302> Molecular and biological characterization of a murine ligand for CD40
<303> Nature
<304> 357

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<307> 1992
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         10                  15                  20

agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt   148
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     25                  30                  35

agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga   196
Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
 40                  45                  50                  55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg   244
Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
                 60                  65                  70

ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga   292
Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
             75                  80                  85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta   340
Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
         90                  95                 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa   388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
    105                 110                 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt   436
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120                 125                 130                 135

cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg   484
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
                140                 145                 150

caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga   532
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
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                155                 160                 165

ggt gcc cct ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga   580
Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly
        170                 175                 180

cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc   628
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro
    185                 190                 195

cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa   676
Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys
200                 205                 210                 215

ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag   724
Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu
                220                 225                 230

gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat   772
Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr
            235                 240                 245

cag aaa gct gca ttg ttc cct gat ggc cat aga aga ttg gat aag gtc   820
Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Val
        250                 255                 260

gaa gag gaa gta aac ctt cat gaa gat ttt gta ttc ata aaa aag cta   868
Glu Glu Glu Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu
    265                 270                 275

aag aga tgc aac aaa gga gaa gga tct tta tcc ttg ctg aac tgt gag   916
Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu
280                 285                 290                 295

gag atg aga agg caa ttt gaa gac ctt gtc aag gat ata acg tta aac   964
Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn
                300                 305                 310

aaa gaa gag aaa aaa gaa aac agc ttt gaa atg caa aga ggt gat gag   1012
Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu
            315                 320                 325

gat cct caa att gca gca cac gtt gta agc gaa gcc aac agt aat gca   1060
Asp Pro Gln Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala
        330                 335                 340

gca tcc gtt cta cag tgg gcc aag aaa gga tat tat acc atg aaa agc   1108
Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser
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    345                 350                 355

aac ttg gta atg ctt gaa aat ggg aaa cag ctg acg gtt aaa aga gaa   1156
Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu
360                 365                 370                 375

gga ctc tat tat gtc tac act caa gtc acc ttc tgc tct aat cgg gag   1204
Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu
                380                 385                 390

cct tcg agt caa cgc cca ttc atc gtc ggc ctc tgg ctg aag ccc agc   1252
Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser
            395                 400                 405

att gga tct gag aga atc tta ctc aag gcg gca aat acc cac agt tcc   1300
Ile Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser
        410                 415                 420

tcc cag ctt tgc gag cag cag tct gtt cac ttg ggc gga gtg ttt gaa   1348
Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu
    425                 430                 435

tta caa gct ggt gct tct gtg ttt gtc aac gtg act gaa gca agc caa   1396
Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln
440                 445                 450                 455

gtg atc cac aga gtt ggc ttc tca tct ttt ggc tta ctc aaa ctc       1441
Val Ile His Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu
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<213> Artificial Sequence
<223> Description of Artificial Sequence: Murine surfactant protein D (except CRD) fused to the extracellular domain of murine CD40 ligand

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             20                  25                  30
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Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
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Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

His Arg Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp
260 265 270

Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser
275 280 285

Leu Ser Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu
290 295 300

Val Lys Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe
305 310 315 320

Glu Met Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val
325 330 335

Ser Glu Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys
340 345 350

Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys
355 360 365

Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val
370 375 380

Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val
385 390 395 400

Gly Leu Trp Leu Lys Pro Ser Ile Gly Ser Glu Arg Ile Leu Leu Lys
405 410 415

Ala Ala Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val
420 425 430

His Leu Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val
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Asn Val Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser
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Phe Gly Leu Leu Lys Leu
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12-13-99

SEQUENCE LISTING

<110> Kornbluth, Richard S

<120> Multimeric forms of CD40L and other TNF family members

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<140> 60/111,471
<141> 1998-12-08

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<223> Mature murine surfactant protein D including hub
region, collagenous portion, and neck, but
excluding carbohydrate recognition domain (CRD)

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stalk.

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the extracellular portion of human CD40L

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<301> Spriggs, Melanie K.
Armitage, Richard J.

Strockbine, L
Clifford, K N.
Macduff, B M.
Sato, T A.
Maliszewski, C R.
Fanslow, William C.
<302> Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion.
<303> J. Exp. Med.
<304> 176
<305> 6
<306> 1543-1550
<307> 1992
<313> 801 TO 1600

<300>
<301> Motwani, M
White, R A.
<302> Mouse surfactant protein-D. cDNA cloning, characterization, and gene localization to chromosome 14.
<303> J. Immunol.
<304> 155
<305> 12
<306> 5671-5677
<307> 1995
<313> 32 TO 800

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Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys
10 15 20

agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt 148
Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
25 30 35

agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga 196
Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
40 45 50 55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg 244
Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
60 65 70

ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga 292
Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
75 80 85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta 340

Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
90 95 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa 388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
105 110 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt 436
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120 125 130 135

cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg 484
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
140 145 150

caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga 532
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
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170 175 180

cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc 628
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185 190 195

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200 205 210 215

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220 225 230

gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat 772
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235 240 245

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Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Ile
250 255 260

gaa gat gaa agg aat ctt cat gaa gat ttt gta ttc atg aaa acg ata 868
Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr Ile
265 270 275

cag aga tgc aac aca gga gaa aga tcc tta tcc tta ctg aac tgt gag 916
Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu
280 285 290 295

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Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu Asn
300 305 310

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Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly Asp
315 320 325

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330 335 340

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345 350 355

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380 385 390

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Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser
410 415 420

tcc gcc aaa cct tgc ggg caa caa tcc att cac ttg gga gga gta ttt 1348
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425 430 435

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440 445 450 455

caa gtg agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc 1444
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surfactant protein D (without the CRD) fused to
the extracellular portion of human CD40L

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Asn Leu Gly Ala Glu Met Lys Ser Leu Ser Gln Arg Ser Val Pro Asn
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Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

His Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
260 265 270

Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
275 280 285

Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
290 295 300

Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
305 310 315 320

Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
325 330 335

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
340 345 350

Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
355 360 365

Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
370 375 380

Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
385 390 395 400

Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
405 410 415

Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
420 425 430

Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
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collagenous portion, and neck, but excluding
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including stalk

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<301> Motwani, M
White, R A.
Guo, N
Dowler, L L.
Tauber, A I.
Motwani, M
<302> Mouse surfactant protein-D. cDNA cloning,
characterization, and gene localization to chromosome
14.
<303> J. Immunol.
<304> 155
<305> 12
<306> 5671-5677
<307> 1995
<313> 32 TO 800

<300>
<301> Anderson, D M.
Maraskovsky, E
Billingsley, W L.
Dougall, W C.
<302> A homologue of the TNF receptor and its ligand enhance
T-cell growth and dendritic-cell function.
<303> Nature
<304> 390
<305> 6656
<306> 175-179
<307> 1997
<313> 801 TO 1534

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Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
40 45 50 55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg 244
Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
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ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga 292
Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
75 80 85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta 340
Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
90 95 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa 388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
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Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
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cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg 484
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140 145 150

caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga 532
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
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185 190 195

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His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr
280 285 290 295

cta cct gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg 964
Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val
300 305 310

cag aag gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct 1012
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315 320 325

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330 335 340

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345 350 355

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Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg
380 385 390

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395 400 405

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Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu
425 430 435

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Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His
440 445 450 455

ttt tat tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa 1444
Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu
460 465 470

gaa att agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa 1492
Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
475 480 485

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Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
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Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys
260 265 270

Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser
275 280 285

Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys
290 295 300

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
305 310 315 320

Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu
325 330 335

Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu
340 345 350

Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu
355 360 365

Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr
370 375 380

Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu
385 390 395 400

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro
405 410 415

Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys
420 425 430

Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp
435 440 445

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
450 455 460

Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro
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Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
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Val Gln Asp Ile Asp
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<223> Description of Artificial Sequence: Murine surfactant protein D (except CRD) fused to the extracellular domain of murine CD40 ligand

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<223> 5' UTR from rat surfactant protein D

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<222> (32)..(1441)

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<221> misc_recomb
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<223> Mature murine surfactant protein D including hub region, collagenous portion, and neck, but excluding carbohydrate recognition domain (CRD)

<220>
<221> misc_feature
<222> (800)..(1441)
<223> Murine CD40 ligand extracellular region, including stalk

<300>
<301> Motwani, M

White, R A.
Guo, N
Dowler, L L.
Tauber, A I.
Motwani, M
<302> Mouse surfactant protein-D. cDNA cloning, characterization, and gene localization to chromosome 14.
<303> J. Immunol.
<304> 155
<305> 12
<306> 5671-5677
<307> 1995
<313> 32 TO 800

<300>
<301> Armitage, R
Fanslow, W
Sato, T A.
Clifford, K N.
<302> Molecular and biological characterization of a murine ligand for CD40
<303> Nature
<304> 357
<305> 6373
<306> 80-82
<307> 1992
<313> 801 TO 1441

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Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys
10 15 20

agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt 148
Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
25 30 35

agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga 196
Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
40 45 50 55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg 244
Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
60 65 70

ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga 292
Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
75 80 85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta 340
Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
90 95 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa 388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
105 110 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt 436
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120 125 130 135

cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg 484
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
140 145 150

caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga 532
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
155 160 165

ggt gcc cct ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga 580
Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly
170 175 180

cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc 628
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro
185 190 195

cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa 676
Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys
200 205 210 215

ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag 724
Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu
220 225 230

gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat 772
Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr
235 240 245

cag aaa gct gca ttg ttc cct gat ggc cat aga aga ttg gat aag gtc 820
Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Val
250 255 260

gaa gag gaa gta aac ctt cat gaa gat ttt gta ttc ata aaa aag cta 868
Glu Glu Glu Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu
265 270 275

aag aga tgc aac aaa gga gaa gga tct tta tcc ttg ctg aac tgt gag 916
Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu
280 285 290 295

gag atg aga agg caa ttt gaa gac ctt gtc aag gat ata acg tta aac 964
Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn

300 305 310

aaa gaa gag aaa aaa gaa aac agc ttt gaa atg caa aga ggt gat gag 1012
Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu
315 320 325

gat cct caa att gca gca cac gtt gta agc gaa gcc aac agt aat gca 1060
Asp Pro Gln Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala
330 335 340

gca tcc gtt cta cag tgg gcc aag aaa gga tat tat acc atg aaa agc 1108
Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser
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Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu
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Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu
380 385 390

cct tcg agt caa cgc cca ttc atc gtc ggc ctc tgg ctg aag ccc agc 1252
Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser
395 400 405

att gga tct gag aga atc tta ctc aag gcg gca aat acc cac agt tcc 1300
Ile Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser
410 415 420

tcc cag ctt tgc gag cag cag tct gtt cac ttg ggc gga gtg ttt gaa 1348
Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu
425 430 435

tta caa gct ggt gct tct gtg ttt gtc aac gtg act gaa gca agc caa 1396
Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln
440 445 450 455

gtg atc cac aga gtt ggc ttc tca tct ttt ggc tta ctc aaa ctc 1441
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<213> Artificial Sequence
<223> Description of Artificial Sequence: Murine surfactant protein D (except CRD) fused to the extracellular domain of murine CD40 ligand

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Asn Leu Gly Ala Glu Met Lys Ser Leu Ser Gln Arg Ser Val Pro Asn
20 25 30

Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

His Arg Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp
260 265 270

Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser
275 280 285

Leu Ser Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu
290 295 300

Val Lys Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe
305 310 315 320

Glu Met Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val
325 330 335

Ser Glu Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys
340 345 350

Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys
355 360 365

Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val
370 375 380

Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val
385 390 395 400

Gly Leu Trp Leu Lys Pro Ser Ile Gly Ser Glu Arg Ile Leu Leu Lys
405 410 415

Ala Ala Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val
420 425 430

His Leu Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val
435 440 445

Asn Val Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser
450 455 460

Phe Gly Leu Leu Lys Leu
465 470